REMARKS

Introduction

Continued examination and favorable reconsideration are respectfully requested. Applicant gratefully appreciates the courtesies extended by the Examiner to Applicant's representative during the personal interview of August 22, 2007. At the interview, exemplary distinctions between the claimed invention and the cited art were discussed.

Claims 1-15, 17, and 20-27 are pending herein. Claims 1-7 and 11 were previously withdrawn, and claims 16 and 18 were previously canceled. The final Office Action dated June 18, 2007, rejected claims 8-10 and 12-27, under 35 U.S.C. §103(a) as being unpatentable over U.S. Patent No. 6,446,010 to Eriksson et al. in view of the publication by Arnold et al., and further in view of the publication by Wilkins et al. Entry of this amendment, reconsideration, and prompt allowance, are respectfully solicited.

Rejection of Claims 8-10 and 12-27 Under 35 U.S.C. §103(a)

At page 2 of the Office Action, claims 8-10 and 12-27 are rejected claims under 35 U.S.C. §103(a) as being unpatentable over Eriksson et al. in view of Arnold et al., and further in view of Wilkins et al. The rejection is respectfully traversed.

Claim 8 recites a method for peptide modification evaluation including features of "b) apportioning [a] spectral range for the at least one modified query peptide into a plurality of mass intervals," and "c) distributing the mass ratios for the fragments of the at least one modified query peptide over one or more of the plurality of mass intervals...." Claim 8 also includes features of

Page 11 of 16

"d) postulating that a modification of one or more fragments within a mass interval has occurred resulting in a modified mass ratio for the one or more fragments," and "e) excluding or adjusting modified mass ratios in the mass interval that correspond to at least one predetermined ion type of the fragments."

Claim 8 likewise includes features of "g) scoring the mass ratio comparisons between the one or more remaining fragments of the at least one modified query peptide versus the at least one known peptide fragmentation spectrum within the mass interval," and "h) repeating steps (d) through (g) for each remaining mass interval of the one or more mass intervals over which mass ratios are distributed in step (c) to generate respective scored mass comparisons for each remaining mass interval." The method of claim 8 therefore includes features of performing a scoring operation using mass ratio comparisons within each mass interval, and repeating enumerated step (d) - (g) for each interval over which mass ratios are distributed. Claim 8 includes further features of "i) summing the scored mass ratio comparisons generated in steps (g) and (h) to generate a summed score for the at least one known peptide fragmentation spectrum over the spectral range," and "j) identifying at least one known peptide best matching the at least one modified query peptide when taking the mass of the modification into account, based on the summed score." Claim 8 therefore includes features of a repeated scoring process within each of a series of mass intervals, and performing a separate summing operation to generate a summed score across the processed mass intervals, to ultimately identify at least one known peptide best matching the subject modified query peptide based on the aggregate summed score.

Neither Eriksson et al., Arnold et al., Wilkins et al., nor their combination, even if

Page 12 of 16

combination were proper, discloses or suggests a method as recited in claim 8. Eriksson et al., as admitted in the Office Action, fails to disclose or suggest peptide modification evaluation that includes features of "distributing the mass ratios for the fragments of the at least one modified query peptide over one or more of the plurality of mass intervals," but instead describes comparison of entire molecular weights, to determine whether a candidate protein identification exceeds a likelihood of matching by a randomized protein composition. See, e.g., Eriksson et al., col. 10, lines 52-65.

Arnold et al., which the Office Action cites to cure the deficiencies of Eriksson et al., describes techniques for comparison of the mass spectra of related bacterial species over intervals. See, e.g., page 635, first column. The matching of those intervals is not based on "postulated" peptide fragment modifications occurring in a given interval. No modifications are taken into account in the comparison. Instead, the fragment weights from two samples in an interval are directly compared to calculate a cross or auto-correction value in each interval (e.g., an "r" value between 0 and 1).

Amold et el. does not in any way suggest features of "g) scoring the mass ratio comparisons between the one or more remaining fragments of the at least one modified query peptide versus the at least one known peptide fragmentation spectrum within the mass interval," nor "h) repeating steps (d) through (g) for each remaining mass interval of the one or more mass intervals over which mass ratios are distributed in step (c) to generate respective scored mass comparisons for each remaining mass interval." The comparison ("r") values derived for the intervals of Arnold et al. are never "summed." That reference describes computing a product of

Page 13 of 16

the comparison values across all intervals. The use of a product of all intervals, in one regard, will cause the presence of a mismatch in just one interval to significantly reduce the overall comparison product score, which is a desired effect when attempting to isolate a number of closely related strains (at least twenty-five e. coli strains in the cited reference) that may differ by just one peptide in one interval. The method of claim 8, on the other hand, includes features of "i) summing the scored mass ratio comparisons generated in steps (g) and (h) to generate a summed score for the at least one known peptide fragmentation spectrum over the spectral range." These additive features can, for example, preserve relatively small but significant differences between close fragment and modification scores, which differences could be obliterated, for instance, by attempting to multiply those scores when even a single interval registers a low score. The purposes and techniques of Arnold et al. do not suggest the features of claim 8.

Wilkins et al. is cited in the Office Action merely to demonstrate post-translational modifications, but suggests no more of the method of claim 8 than Eriksson et al. and Arnold et al. Claim 8 distinguishes over Eriksson et al., Arnold et al., Wilkins et al., and their combination, even if combination were proper. The rejection of claim 8 based on those references is overcome and should be withdrawn. Reconsideration is respectfully requested.

Claims 16 and 18 are canceled. Claims 9-10, 12-15, 17, and 19-27 distinguish over Eriksson et al., Arnold et al., Wilkins et al., and their combination, even if combination were proper, for at least the same reasons as claim 8 does, from which those claims depend. The

Page 14 of 16

Application No. 10/087,541

Amendment dated September 18, 2007

Response to Office Action dated June 18, 2007

rejection of those claims is overcome and should be withdrawn. Reconsideration is respectfully

requested.

Rejection of Claims 8-10 and 12-19 for Obviousness-Type Double Patenting

The Office Action maintained the provisional rejection of claims 8-10 and 12-19 under the

judicially created doctrine of obviousness-type double patenting as being unpatentable over the

claims of copending Application No. 10/241,751. Claims 16 and 18 are canceled. Applicant

respectfully traverses the provisional double-patenting rejection of claims 9, 10, 12-15, 17, and 19,

including for all the reasons stated in the amendment filed March 13, 2006. Applicant reiterates

that should this rejection be maintained, applicant will consider the filing of a Terminal Disclaimer

as appropriate upon indication that the claims of the present application are otherwise allowable.

CONCLUSION

In view of the foregoing amendments and remarks, applicant respectfully requests favorable

reconsideration of the present application and a timely allowance of the pending claims.

Should the Examiner deem that any further action by applicant or applicant's undersigned

representative is desirable and/or necessary, the Examiner is invited to telephone the undersigned

at the number set forth below.

Page 15 of 16

If there are any other fees due in connection with the filing of this response, please charge the fees to deposit Account No. 50-0925. If a fee is required for an extension of time under 37 C.F.R. § 1.136 not accounted for above, such extension is requested and should also be charged to said Deposit Account.

Respectfully submitted,

Leonard D. Bowersox Reg. No. 33,226

KILYK & BOWERSOX, P.L.L.C.

3603-E Chain Bridge Road Fairfax, Virginia 22030

Tel.: (703) 385-9688

Fax.: (703) 385-9719